RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/643,836_

Source: _____

Date Processed by STIC: _____

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RAW SEQUENCE LISTING   DATE: 01/11/2005
PATENT APPLICATION: US/10/643,836   TIME: 12:22:35

Input Set : N:\Crf3\RULE60\10643836.RAW.txt
Output Set: N:\CRF4\01112005\J643836.raw

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  1 <110> APPLICANT: Dumas Milne Edwards, Jean Baptiste
  2        Bougueleret, Lydie
  3       .Jobert, Severin
  4 <120> TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED
PROTEINS
  5 <130> FILE REFERENCE: 78.US3.REG
  6 <140> CURRENT APPLICATION NUMBER: 10/643,836
  7 <141> CURRENT FILING DATE: 2003-08-19
  8 <150> PRIOR APPLICATION NUMBER: US/09/731,872
  9 <151> PRIOR FILING DATE: 2000-12-07
 10 <150> PRIOR APPLICATION NUMBER: US 60/169,629
 11 <151> PRIOR FILING DATE: 1999-12-08
 12 <150> PRIOR APPLICATION NUMBER: US 60/187,470
 13 <151> PRIOR FILING DATE: 2000-03-06
 14 <160> NUMBER OF SEQ ID NOS: 482
 15 <170> SOFTWARE: Patent.pm
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2201
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: 169..1692
 24 <221> NAME/KEY: sig_peptide
 25 <222> LOCATION: 169..249
 26 <223> OTHER INFORMATION: Von Heijne matrix
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 28        seq VLLLLLLERGMFS/SP
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 30        agatgtgaat agctccacta taccagcctc gtcttccttc cgggggacaa cgtgggtcag        60
 31        ggcacagaga gatatttaat gtcaccctct tggggctttc atgggactcc ctctgccaca       120
 32        tttttggag gttgggaaag ttgctagagg cttcagaact ccagccta atg gat ccc        177
 33                                                              Met Asp Pro
 34                                                              -25
 35        aaa ctc ggg aga atg gct gcg tcc ctg ctg gct gtg ctg ctg ctg ctg       225
 36        Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu Leu Leu Leu
 37                        -20             -15                 -10
 38        ctg ctg gag cgc ggc atg ttc tcc tca ccc tcc ccg ccc ccg gcg ctg       273
 39        Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro Pro Ala Leu
 40                        -5              1               5
 41        tta gag aaa gtc ttc cag tac att gac ctc cat cag gat gaa ttt gtg       321
 42        Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His Gln Asp Glu Phe Val
 43            10              15                  20
 44        cag acg ctg aag gag tgg gtg gcc atc gag agc gac tct gtc cag cct       369
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45   Gln Thr Leu Lys Glu Trp Val Ala Ile Glu Ser Asp Ser Val Gln Pro
46   25              30              35                  40
47   gtg cct cgc ttc aga caa gag ctc ttc aga atg atg gcc gtg gct gcg    417
48   Val Pro Arg Phe Arg Gln Glu Leu Phe Arg Met Met Ala Val Ala Ala
49               45              50                  55
50   gac acg ctg cag cgc ctg ggg gcc cgt gtg gcc tcg gtg gac atg ggt    465
51   Asp Thr Leu Gln Arg Leu Gly Ala Arg Val Ala Ser Val Asp Met Gly
52               60              65                  70
53   cct cag cag ctg ccc gat ggt cag agt ctt cca ata cct ccc gtc atc    513
54   Pro Gln Gln Leu Pro Asp Gly Gln Ser Leu Pro Ile Pro Pro Val Ile
55               75              80                  85
56   ctg gcc gaa ctg ggg agc gat ccc acg aaa ggc acc gtg tgc ttc tac    561
57   Leu Ala Glu Leu Gly Ser Asp Pro Thr Lys Gly Thr Val Cys Phe Tyr
58       90              95                  100
59   ggc cac ttg gac gtg cag cct gct gac cgg ggc gat ggg tgg ctc acg    609
60   Gly His Leu Asp Val Gln Pro Ala Asp Arg Gly Asp Gly Trp Leu Thr
61   105             110             115                 120
62   gac ccc tat gtg ctg acg gag gta gac ggg aaa ctt tat gga cga gga    657
63   Asp Pro Tyr Val Leu Thr Glu Val Asp Gly Lys Leu Tyr Gly Arg Gly
64               125             130                 135
65   gcg acc gac aac aaa ggc cct gtc ttg gct tgg atc aat gct gtg agc    705
66   Ala Thr Asp Asn Lys Gly Pro Val Leu Ala Trp Ile Asn Ala Val Ser
67               140             145                 150
68   gcc ttc aga gcc ctg gag caa gat ctt cct gtg aat atc aaa ttc atc    753
69   Ala Phe Arg Ala Leu Glu Gln Asp Leu Pro Val Asn Ile Lys Phe Ile
70       155             160                 165
71   att gag ggg atg gaa gag gct ggc tct gtt gcc ctg gag gaa ctt gtg    801
72   Ile Glu Gly Met Glu Glu Ala Gly Ser Val Ala Leu Glu Glu Leu Val
73       170             175                 180
74   gaa aaa gaa aag gac cga ttc ttc tct ggt gtg gac tac att gta att    849
75   Glu Lys Glu Lys Asp Arg Phe Phe Ser Gly Val Asp Tyr Ile Val Ile
76   185             190             195                 200
77   tca gat aac ctg tgg atc agc caa agg aag cca gca atc act tat gga    897
78   Ser Asp Asn Leu Trp Ile Ser Gln Arg Lys Pro Ala Ile Thr Tyr Gly
79               205             210                 215
80   acc cgg ggg aac agc tac ttc atg gtg gag gtg aaa tgc aga gac cag    945
81   Thr Arg Gly Asn Ser Tyr Phe Met Val Glu Val Lys Cys Arg Asp Gln
82               220             225                 230
83   gat ttt cac tca gga acc ttt ggt ggc atc ctt cat gaa cca atg gct    993
84   Asp Phe His Ser Gly Thr Phe Gly Gly Ile Leu His Glu Pro Met Ala
85       235             240                 245
86   gat ctg gtt gct ctt ctc ggt agc ctg gta gac tcg tct ggt cat atc   1041
87   Asp Leu Val Ala Leu Leu Gly Ser Leu Val Asp Ser Ser Gly His Ile
88       250             255                 260
89   ctg gtc cct gga atc tat gat gaa gtg gtt cct ctt aca gaa gag gaa   1089
90   Leu Val Pro Gly Ile Tyr Asp Glu Val Val Pro Leu Thr Glu Glu Glu
91   265             270             275                 280
92   ata aat aca tac aaa gcc atc cat cta gac cta gaa gaa tac cgg aat   1137
93   Ile Asn Thr Tyr Lys Ala Ile His Leu Asp Leu Glu Glu Tyr Arg Asn
```

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94                    285                 290                 295
95     agc agc cgg gtt gag aaa ttt ctg ttc gat act aag gag gag att cta     1185
96     Ser Ser Arg Val Glu Lys Phe Leu Phe Asp Thr Lys Glu Glu Ile Leu
97                    300                 305                 310
98     atg cac ctc tgg agg tac cca tct ctt tct att cat ggg atc gag ggc     1233
99     Met His Leu Trp Arg Tyr Pro Ser Leu Ser Ile His Gly Ile Glu Gly
100                   315                 320                 325
101     gcg ttt gat gag cct gga act aaa aca gtc ata cct ggc cga gtt ata    1281
102     Ala Phe Asp Glu Pro Gly Thr Lys Thr Val Ile Pro Gly Arg Val Ile
103                   330                 335                 340
104     gga aaa ttt tca atc cgt cta gtc cct cac atg aat gtg tct gcg gtg    1329
105     Gly Lys Phe Ser Ile Arg Leu Val Pro His Met Asn Val Ser Ala Val
106     345                   350                 355                 360
107     gaa aaa cag gtg aca cga cat ctt gaa gat gtg ttc tcc aaa aga aat    1377
108     Glu Lys Gln Val Thr Arg His Leu Glu Asp Val Phe Ser Lys Arg Asn
109                   365                 370                 375
110     agt tcc aac aag atg gtt gtt tcc atg act cta gga cta cac ccg tgg    1425
111     Ser Ser Asn Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp
112                   380                 385                 390
113     att gca aat att gat gac acc cag tat ctc gca gca aaa aga gcg atc    1473
114     Ile Ala Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile
115                   395                 400                 405
116     aga aca gtg ttt gga aca gaa cca gat atg atc cgg gat gga tcc acc    1521
117     Arg Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr
118                   410                 415                 420
119     att cca att gcc aaa atg ttc cag gag atc gtc cac aag agc gtg gtg    1569
120     Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val Val
121     425                   430                 435                 440
122     cta att ccg ctg gga gct gtt gat gat gga gaa cat tcg cag aat gag    1617
123     Leu Ile Pro Leu Gly Ala Val Asp Asp Gly Glu His Ser Gln Asn Glu
124                   445                 450                 455
125     aaa atc aac agg tgg aac tac ata gag gga acc aaa tta ttt gct gcc    1665
126     Lys Ile Asn Arg Trp Asn Tyr Ile Glu Gly Thr Lys Leu Phe Ala Ala
127                   460                 465                 470
128     ttt ttc tta gag atg gcc cag ctc cat taatcacaag aaccttctag          1712
129     Phe Phe Leu Glu Met Ala Gln Leu His
130                   475                 480
131     tctgatctga tccactgaca gattcacctc ccccacatcc ctagacaggg atggaatgta  1772
132     aatatccaga gaatttgggt ctagtatagt acattttccc ttccatttaa aatgtcttgg  1832
133     gatatctgga tcagtaataa aatatttcaa aggcacagat gttggaaatg gtttaaggtc  1892
134     ccccactgca caccttcctc aagtcatagc tgcttgcagc aacttgattt ccccaagtcc  1952
135     tgtgcaatag ccccaggatt ggattccttc caaccttta gcatatctcc aaccttgcaa    2012
136     tttgattggc ataatcactc cagtttgctt tctaggtcct caagtgctcg tgacacataa   2072
137     tcattccatc caatgatcgc ctttgcttta ccactctttc cttttatctt attaataaaa   2132
138     atgttggtct ccaccactga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaagaaaaaa    2192
139     aaaaaaaaa                                                          2201
141  <210> SEQ ID NO: 2
142  <211> LENGTH: 1631
143  <212> TYPE: DNA
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145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: 148..1140
148 <221> NAME/KEY: sig_peptide
149 <222> LOCATION: 148..240
150 <223> OTHER INFORMATION: Von Heijne matrix
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152       seq LVLLLVTRSPVNA/CL
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155       cttggaccct ccccctcgct tctcgttcta ctgccccagg agcccggcgg tccgggact    120
156       cccgtccgtg ccggtgcggg cgccggc atg tgg ctg tgg gag gac cag ggc ggc    174
157                                   Met Trp Leu Trp Glu Asp Gln Gly Gly
158                                   -30                     -25
159       ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg    222
160       Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr
161            -20                 -15                 -10
162       cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta    270
163       Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu
164            -5                  1              5                    10
165       ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag    318
166       Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln
167                     15                  20                  25
168       gtg ctc aag ccc cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc    366
169       Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly
170                     30                  35                  40
171       agc cac gac gcg ccc gag aac acg ctg gcg gcc att cgg cag gca gct    414
172       Ser His Asp Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala
173                45                  50                  55
174       aag aat gga gca aca ggc gtg gag ttg gac att gag ttt act tct gac    462
175       Lys Asn Gly Ala Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp
176            60                  65                  70
177       ggg att cct gtc tta atg cac gat aac aca gta gat agg acg act gat    510
178       Gly Ile Pro Val Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp
179       75                  80                  85                  90
180       ggg act ggg cga ttg tgt gat ttg aca ttt gaa caa att agg aag ctg    558
181       Gly Thr Gly Arg Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu
182                     95                  100                 105
183       aat cct gca gca aac cac aga ctc agg aat gat ttc cct gat gaa aag    606
184       Asn Pro Ala Ala Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys
185                     110                 115                 120
186       atc cct acc cta atg gaa gct gtt gca gag tgc cta aac cat aac ctc    654
187       Ile Pro Thr Leu Met Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu
188                     125                 130                 135
189       aca atc ttc ttt gat gtc aaa ggc cat gca cac aag gct act gag gct    702
190       Thr Ile Phe Phe Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala
191            140                 145                 150
192       cta aag aaa atg tat atg gaa ttt cct caa ctg tat aat aat agt gtg    750
```

```
193      Leu Lys Lys Met Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val
194      155             160             165             170
195      gtc tgt tct ttc ttg cca gaa gtt atc tac aag atg aga caa aca gat    798
196      Val Cys Ser Phe Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp
197                      175             180             185
198      cgg gat gta ata aca gca tta act cac aga cct tgg agc cta agc cat    846
199      Arg Asp Val Ile Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His
200                      190             195             200
201      aca gga gat ggg aaa cca cgc tat gat act ttc tgg aaa cat ttt ata    894
202      Thr Gly Asp Gly Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile
203              205             210             215
204      ttt gtt atg atg gac att ttg ctc gat tgg agc atg cat aat atc ttg    942
205      Phe Val Met Met Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu
206          220             225             230
207      tgg tac ctg tgt gga att tca gct ttc ctc atg caa aag gat ttt gta    990
208      Trp Tyr Leu Cys Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val
209      235             240             245             250
210      tcc ccg gcc tac ttg aag aag tgg tca gct aaa gga atc cag gtt gtt   1038
211      Ser Pro Ala Tyr Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val
212                      255             260             265
213      ggt tgg act gtt aat acc ttt gat gaa aag agt tac tac gaa tcc cat   1086
214      Gly Trp Thr Val Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His
215                      270             275             280
216      ctt ggt tcc agc tat atc act gac agc atg gta gaa gac tgc gaa cct   1134
217      Leu Gly Ser Ser Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro
218              285             290             295
219      cac ttc tagactttca cggtgggacg aaacgggttc agaaactgcc aggggcctca   1190
220      His Phe
221          300
222      tacagggata tcaaaatacc ctttgtgcta gcccaggccc tggggaatca ggtgactcac   1250
223      acaaatgcaa tagttggtca ctgcattttt acctgaacca aagctaaacc cggtgttgcc   1310
224      accatgcacc atggcatgcc agagttcaac actgttgctc ttgaaaatct ggggtctgaa   1370
225      aaaacgcaca agagcccctg ccctgcccta gctgaggcac acagggagac ccagtgagga   1430
226      taagcacaga ttgaattgta caatttgcag atgcagatgt aaatgcatgg gacatgcatg   1490
227      ataactcaga gttgacattt taaaacttgc cacacttatt tcaaatattt gtactcagct   1550
228      atgttaacat gtactgtaga catcaaactt gtggccatac taataaaatt attaaaagga   1610
229      gcacaaaaaa aaaaaaaaaa a                                             1631
231 <210> SEQ ID NO: 3
232 <211> LENGTH: 1245
233 <212> TYPE: DNA
234 <213> ORGANISM: Homo sapiens
235 <220> FEATURE:
236 <221> NAME/KEY: CDS
237 <222> LOCATION: 85..906
238 <221> NAME/KEY: sig_peptide
239 <222> LOCATION: 85..135
240 <223> OTHER INFORMATION: Von Heijne matrix
241      score 3.86022363031904
242      seq GFVAALVAGGVAG/VS
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RAW SEQUENCE LISTING ERROR SUMMARY        DATE: 01/11/2005
PATENT APPLICATION:  US/10/643,836        TIME: 12:22:36

Input Set : N:\Crf3\RULE60\10643836.RAW.txt
Output Set: N:\CRF4\01112005\J643836.raw
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:12; Xaa Pos. 44,45
Seq#:20; N Pos. 989
Seq#:45; Xaa Pos. 132
Seq#:97; Xaa Pos. 21
Seq#:103; Xaa Pos. 185
Seq#:104; N Pos. 972
Seq#:115; Xaa Pos. 41
Seq#:135; N Pos. 347
Seq#:135; Xaa Pos. 47
Seq#:137; Xaa Pos. 50,51
Seq#:165; N Pos. 1707
Seq#:188; N Pos. 871
Seq#:202; N Pos. 483
Seq#:207; Xaa Pos. 113,114,115
Seq#:210; Xaa Pos. 76
Seq#:220; Xaa Pos. 95
Seq#:253; Xaa Pos. 44,45
Seq#:286; Xaa Pos. 132
Seq#:338; Xaa Pos. 21
Seq#:344; Xaa Pos. 185
Seq#:356; Xaa Pos. 41
Seq#:376; Xaa Pos. 47
Seq#:378; Xaa Pos. 50,51
Seq#:448; Xaa Pos. 113,114,115
Seq#:451; Xaa Pos. 76
Seq#:461; Xaa Pos. 95
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Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:1; Line(s) 4
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VERIFICATION SUMMARY   DATE: 01/11/2005
PATENT APPLICATION: **US/10/643,836**   TIME: 12:22:36

Input Set : **N:\Crf3\RULE60\10643836.RAW.txt**
Output Set: **N:\CRF4\01112005\J643836.raw**

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L:29 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:153 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:243 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:318 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:417 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:460 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:551 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:650 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:747 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:794 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:850 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:896 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:915 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:412
L:956 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:1005 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:1104 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:1170 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
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L:1293 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:1396 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:1446 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1449 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:966
L:1516 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:1549 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:1589 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
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L:2142 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
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L:2893 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
L:3002 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:43
L:3106 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:44
L:3191 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:45
L:3225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:654
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VERIFICATION SUMMARY   DATE: 01/11/2005
PATENT APPLICATION: US/10/643,836   TIME: 12:22:36

Input Set : **N:\Crf3\RULE60\10643836.RAW.txt**
Output Set: **N:\CRF4\01112005\J643836.raw**

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L:3384 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:47
L:3481 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:48
L:3529 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:49
L:3572 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:50
L:6456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97 after pos.:144
L:6752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:923
L:6821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:935
L:7430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:369
L:8386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135 after pos.:310
M:341 Repeated in SeqNo=135
L:8471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:253
M:341 Repeated in SeqNo=137
L:10269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:165 after pos.:1691
L:11620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188 after pos.:830
L:12113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202 after pos.:465
L:12300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:207 after pos.:445
L:12472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:210 after pos.:352
L:13039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:220 after pos.:402
L:14556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:253 after pos.:64
L:15877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:286 after pos.:144
L:17668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:338 after pos.:32
L:17827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:344 after pos.:192
L:18185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:356 after pos.:64
L:18728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:376 after pos.:64
L:18780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:378 after pos.:48
M:341 Repeated in SeqNo=378
L:20843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:448 after pos.:112
L:20937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:451 after pos.:64
L:21264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:461 after pos.:80
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